**Shewanella irciniae** sp. nov., a novel member of the family *Shewanellaceae*, isolated from the marine sponge *Ircinia dendroides* in the Bay of Villefranche, Mediterranean Sea

On On Lee, 1 Stanley C. K. Lau, 2 Mandy M. Y. Tsoi, 1 Xiancui Li, 1 Ioulia Plakhotnikova, 1 Sergey Dobretsov, 1 Madeline C. S. Wu, 1 Po-Keung Wong, 3 Markus Weinbauer 4 and Pei-Yuan Qian 1

Correspondence
Pei-Yuan Qian
boqianpy@ust.hk

1Coastal Marine Laboratory/Department of Biology, The Hong Kong University of Science and Technology, Clear Water Bay, Kowloon, Hong Kong SAR, People’s Republic of China
2Division of Environmental Science and Engineering, The National University of Singapore, Singapore
3Department of Biology, The Chinese University of Hong Kong, Shatin, N. T., Hong Kong SAR, People’s Republic of China
4Microbial Ecology and Biogeochemistry Group, Laboratoire d’Océanographie de Villefranche-sur-Mer, Villefranche-sur-Mer, France

Strain UST040317-058T, comprising non-pigmented, rod-shaped, facultatively anaerobic, Gram-negative cells that are motile by means of single polar flagella, was isolated from the surface of a marine sponge (*Ircinia dendroides*) collected from the Mediterranean Sea. Comparative 16S rRNA gene sequence-based phylogenetic analysis placed the strain in a separate cluster with the recognized bacterium *Shewanella algae* IAM 14159T, with which it showed a sequence similarity of 95–90 %. The sequence similarity between strain UST040317-058T and its other (six) closest relatives ranged from 91–6 to 93-8 %. Strain UST040317-058T showed oxidase, catalase and gelatinase activities. The typical respiratory quinones for shewanellas, menaquinone MK-7 and ubiquinones Q-7 and Q-8, were also detected. The predominant fatty acids in strain UST040317-058T were i15 : 0, 16 : 0, 17 : 1v8c and summed feature 3 (comprising i15 : 0 2-OH and/or 16 : 1v7c), altogether representing 56–9 % of the total. The DNA G+C content was 39–9 mol%.

The strain could be differentiated from other *Shewanella* species by its inability to reduce nitrate or produce H2S and by 10–22 additional phenotypic characteristics. On the basis of the phylogenetic and phenotypic data presented in this study, strain UST040317-058T represents a novel species in the genus *Shewanella*, for which the name *Shewanella irciniae* sp. nov. is proposed. The type strain is UST040317-058T ( = JCM 13528T = NRRL B-41466T).

The family *Shewanellaceae* was established from the emended description of a group of marine *Alteromonas*-like bacteria because of their deep phylogenetic branching and lack of association with any other genus in the family *Alteromonadaceae* (Ivanova et al., 2004c). At present, the family *Shewanellaceae* includes only one genus, *Shewanella* (MacDonell & Colwell, 1985), which was created from the reclassification of two species previously assigned to the genus *Alteromonas*, namely *Alteromonas* putrefaciens (Lee et al., 1981) and *[Alteromonas] hanedai* (Jensen et al., 1980). *Shewanella* species comprise Gram-negative, straight or curved rod-shaped, aerobic or facultatively anaerobic and readily cultivated gammaproteobacteria isolated from diverse sources, including activated sludge (Xu et al., 2005), marine invertebrates (Ivanova et al., 2004b), red algae (Simidu et al., 1990), a tidal flat (Yoon et al., 2004a), seawater (Ivanova et al., 2001, 2004a; Yoon et al., 2004b), sediments (Venkateswaran et al., 1998) and clinical samples (Levin, 1972; Debois et al., 1975; Holmes et al., 1975). In the last decade, the number of recognized species in this genus has increased; they have been studied extensively because of their capacity for dissimilatory reduction of manganese and iron oxides (Myers & Nealson, 1988; Bowman et al., 1997; Venkateswaran et al., 1998), for co-metabolization of...
halogenated organic pollutants (Petrovskis et al., 1994), for the destructive souring of crude petroleum (Semple & Westlake, 1987) and for the production of tetrodotoxin (Simidu et al., 1990) and large proportions of polyunsaturated fatty acids (Bowman et al., 1997; Russell & Nichols, 1999; Ivanova et al., 2004a). At the time of writing, there are more than 30 Shewanella species with validly published names. On the basis of the polyphasic taxonomic data presented in this study, we propose a novel member of this genus, strain UST040317-058T, isolated in March 2004 from the surface of a marine sponge (Ircinia dendroides) found associated with sea-grass (Posidonia) in the Bay of Villefranche in the Mediterranean Sea.

Strain UST040317-058T was isolated using a standard dilution plating technique on a marine agar medium containing 3 g yeast extract (Oxoid), 5 g peptone (Oxoid) and 12 g bacteriological agar (Oxoid) in 1 l 0.22 μm-filtered seawater at 32% salinity after 48 h incubation at 28°C. Unless otherwise indicated, all characteristics described hereafter are based on cultures grown on marine agar under these conditions. Colonies of strain UST040317-058T were milky, raised and circular (0.8–1.5 mm in diameter) with entire edges and a smooth surface (as observed under a Leica MZ6 light microscope at 40× magnification). Gram stain was determined using light microscopy according to Smibert & Krieg (1994). Cell morphology was examined using scanning electron microscopy (6700F; JEOL) according to Neu et al. (2001) and the presence of flagella was determined by transmission electron microscopy according to Allan et al. (2002). Gliding motility was observed under a phase-contrast light microscope (BX51; Olympus) at 100× magnification using cells grown on quarter-strength marine broth 2216 (Oxoid) solidified with 1.2% agar according to Bowman (2000). Strain UST040317-058T comprised Gram-negative, rod-shaped cells that were motile by means of a single polar flagellum (see Supplementary Fig. S1 available in IJSEM Online).

The almost-complete 16S rRNA gene sequence of strain UST040317-058T (1462 bp) was obtained bidirectionally with three replicates, as described by Lau et al. (2004). Comparative analysis of the 16S rRNA gene sequence with sequences deposited in GenBank using BLAST indicated that the strain belonged to the family Shewanellaceae and showed the highest sequence similarity (95.0%) with Shewanella algae IAM 14159T (Simidu et al., 1990). The 16S rRNA gene sequence was automatically, and then manually, aligned with a database of >30,000 previously aligned 16S rRNA gene sequences by using the ARB software package (Ludwig et al., 2004). Phylogenetic trees were constructed using three different methods: neighbour-joining, maximum-likelihood and maximum-parsimony. The neighbour-joining phylogenetic tree (Fig. 1) placed strain UST040317-058T...
within a cluster of two undescribed bacteria which were also isolated from marine sponges: an unidentified sponge bacterium, strain Ex6 (Wichels et al., 2006), and Shewanella species strain HJ039 (GenBank accession no. DQ167234). This cluster, together with the recognized species S. algae IAM 14159T, formed a distinct clade that clustered robustly with another clade comprising six other Shewanella species with validly published names, including Shewanella amazonsensis SB2T (Venkateswaran et al., 1998), Shewanella waksmanii KMM 3823T (Ivanova et al., 2003), Shewanella aquimarina SW-120T (Yoon et al., 2004b), Shewanella marinflava SW-117T (Yoon et al., 2004b), Shewanella colwelliana ATCC 39565T (Coyne et al., 1989) and Shewanella affinis KMM 3587T (Ivanova et al., 2004b). These species shared 91-6–93-8% 16S rRNA gene sequence similarity with strain UST040317-058T. The maximum-likelihood and maximum-parsimony trees based on cladistic methods (i.e. character-based) showed similar topography for the novel strain and the Shewanella species. These results support the inclusion of strain UST040317-058T as a novel species in the genus Shewanella.

The cellular fatty acid profile of strain UST040317-058T was determined using the Sherlock Microbial Identification System (MIDI) according to the manufacturer's protocol. Strain UST040317-058T had a cellular fatty acid profile dominated by the saturated straight-chain fatty acid 16:0 (13.0%), the saturated branched-chain fatty acid i15:0 (14.1%), the unsaturated straight-chain fatty acid 17:1o8c (13.3%) and summed feature 3 (comprising i15:0 2-OH and/or 16:1o7c) (16.3%), which together constituted 56.9% of the total fatty acid content (Table 1). These fatty acids are common to Shewanella species, supporting the inclusion of strain UST040317-058T in the genus. However, some fatty acids that were common in some Shewanella species, e.g. 15:0, 16:1o7c (Table 1) and polyunsaturated fatty acids (Bowman et al., 1997; Skerratt et al., 2002; Ivanova et al., 2004a), were not observed in strain UST040317-058T, suggesting that this novel isolate is unique.

The DNA G+C content of UST040317-058T was 40.0±0.1 mol% (n = 3) as determined using an HPLC method according to Mesbah et al. (1989). This value is within the range of G+C contents observed among members of the genus Shewanella (39.0–54.0 mol%) (Table 2). The presence of respiratory quinones was checked using an HPLC method according to Collins (1994). Menaquinoins extracted from Cellulophaga lytica (Nagawa & Yamasato, 1993) and Pedobacter heparinus (Steyn et al., 1998) served as references for MK-6 and MK-7, respectively, while ubiquinones extracted from Escherichia coli strain XL1-Blue (Gao et al., 2004) served as references for Q-7 and Q-8. MK-7, Q-7 and Q-8, but not MK-6, were detected in strain UST040317-058T.

The oxygen requirement for growth was investigated using the Oxoid Anaerobic System. Growth at different temperatures (4, 12, 20, 28, 36, 44 and 52 °C) and pH (5, 6, 7, 8, 9 and 10) was monitored on marine agar incubated for up to 10 days. The NaCl requirement for growth was tested on a 1·2% agar medium containing 5 g peptone, 5 g MgCl₂, 2 g MgSO₄, 1 g KCl, 0·5 g CaCl₂ and different amounts of NaCl (from 0 up to 180 g) and the pH was adjusted to 7·5 using KOH (Isnansetyo & Kamei, 2003). Haemolytic activity was studied on blood agar containing 40 g blood agar base (Oxoid), 50 ml rabbit blood and 950 ml 0·22 µm-filtered seawater (Ivanova et al., 2004b). Susceptibility to the antibiotics streptomycin, benzylpenicillin, chloramphenicol, ampicillin, tetracycline and kanamycin was tested using standard agar disc diffusion assays according to Acar (1980). The amounts of antibiotic tested ranged from 1·0 to 100·0 µg per disc. The hydrolysis of casein and cellulose was investigated according to Norris et al. (1985) and Bowman (2000), respectively. The hydrolysis of Tweens 20, 40 and 80 and of chitin was tested as described in Baumann & Baumann (1981). The hydrolysis of agar, DNA and starch and the production of oxidase and catalase were determined according to Smibert & Krieg (1994). Other enzymic activities, the utilization of (and acid production from) different carbon sources, the reduction of nitrate and the production of H₂S, indole and acetoin were tested using the commercial systems API 20E, API 20NE, API 50 CH, API ZYM (bioMérieux) and MicroLog 3 (Biolog) according to the manufacturers’ manuals, except that the cells used for the API system were suspended in sterile seawater at 22°C salinity before inoculation (MacDonell et al., 1982). Growth on glycerol, D-glucose, sucrose, D-mannitol, D-galactose, starch, D-sorbitol, D-arabinose and D-melibiose as sole carbon sources was also tested on a 1·2% agar medium containing 0·2 g NaNO₃, 0·2 g NH₄Cl, 0·05 g yeast extract and 4 % (w/v) carbon source in 1 l seawater at 35°C salinity (Nedashkovskaya et al., 2003). Detailed physiological and biochemical characteristics of UST040317-058T are given in the species description below.

Strain UST040317-058T can be differentiated from its closest relative, S. algae IAM 14159T, by means of several phenotypic characteristics, including the inability of the novel strain to reduce nitrate, produce H₂S, grow at 8% NaCl and 40 °C, produce lipase or utilize D-maltose, DL-lactate, DL-malate, succinate, fumarate and L-serine and its ability to utilize D-galactose, D-glucose, D-mannitol and D-sorbitol as sole carbon sources. The novel strain is differentiated from other selected Shewanella species in Table 2. On the basis of the phylogenetic evidence together with the phenotypic characteristics presented in this study, strain UST040317-058T represents a novel species within the genus Shewanella, for which the name Shewanella ircinia sp. nov. is proposed.

**Description of Shewanella ircinia sp. nov.**

*Shewanella ircinia* (ir.ci.ni.ae. N.L. gen. n. *irciniae* of/from *Ircinia*, isolated from the marine sponge *Ircinia dendroides*).

Cells are Gram-negative, short, straight rods (1·3–2·0 µm in length and 0·5 µm in width) and are motile by means of a
Table 1. Cellular fatty acid content of strain UST040317-058\textsuperscript{T} and its close relatives in the genus *Shewanella*

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<td>15.9</td>
<td>18.6</td>
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*Summed feature 1 comprises 13:0 3-OH and/or i15:1.
†Summed feature 2 comprises 14:0 3-OH and/or i16:1.
‡Summed feature 3 comprises i15:0 2-OH and/or 16:1o7c.

The single polar flagellum. Facultatively anaerobic. When cultivated on marine agar at 28 °C for 48 h, colonies are milky, 0.8–1.5 mm in diameter, circular and raised with a smooth surface and an entire edge. Does not produce diffusible pigments. Optimal growth occurs at 20–28 °C, but no growth occurs at temperatures lower than 12 °C or higher than 36 °C. Growth occurs at pH 6–10, but no growth occurs at or below pH 5. Requires NaCl (2.0–6.0% optimum, 2.0–4.0% for growth). MK-7, Q-7 and Q-8 are the predominant respiratory quinones detected. The predominant fatty acids are i15:0, 16:0, 17:1o8c and summed feature 3 (comprising i15:0 2-OH and/or
Table 2. Phenotypic characteristics that differentiate strain UST04317-058T from the seven most closely related members of the genus *Shewanella*

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<td>52</td>
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<td>6 % NaCl</td>
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*The colour of the pigment was brown/greenish.

The type strain, UST04317-058T (=JCM 13528T = NRRRL B-41466T), was isolated from the surface of a marine sponge (*Ircinia dendroides*) associated with *Posidonia* sea-grass in the Bay of Villefranche, Mediterranean Sea.

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**References**


